Factors Influencing Genetic Evaluations of Linebred Hereford Cattle in Diverse Environments[1]

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ABSTRACT: Data from four closely related Line 1 Hereford herds were used to estimate variance components and predict EPD for birth weight (BWT), weaning weight (WWT), and postweaning gain (PWG). Herds were located in diverse environments and differed in level of phenotypic performance. Within-herd BWT analyses considered effects of inbreeding of calf and dam, sex, age of dam (AOD), and contemporary group as fixed and direct and maternal additive genetic effects and permanent environmental effects due to dam as random. The model for WWT included these effects and age of calf. The model for PWG included inbreeding of calf, contemporary group, and direct additive genetic effects. Across-herd analyses were conducted with additional models. The first considered herd-specific inbreeding, sex, and AOD effects. A second model pooled these effects across herds, and a third included pooled sex and AOD effects but ignored inbreeding. Across-herd EPD, including and ignoring inbreeding, were predicted for WWT preadjusted with standard adjustments for Hereford cattle. Within-herd analyses indicated potential for heterogenous genetic and environmental variances across herds. Across-herd variance component estimates were consistent, regardless of the model. Estimates of genetic trends indicated potential for bias in genetic evaluations resulting from choice of model. Differences in magnitude of fixed effects between herds were observed. Genetic evaluations were different when pooled or herd-specific fixed effects were used. Allowance for individual herd differences in fixed effects in across-herd evaluations is suggested.

Key Words: Beef Cattle, Genetic Analysis, Linear Models

J. Anim. Sci. 1996. 74:1499–1510

Introduction

Expected progeny differences from national cattle evaluations (**NCE**) that use BLUP methodology (Henderson, 1973) are generally accepted as the most reliable predictions of genetic merit available. These predictions are made with statistical models that may not adequately address peculiarities of individual herds. The assumption of homogeneous (co)variances across herds and use of a priori correction for some fixed effects may affect evaluation of individuals in some herds.

Within-herd evaluation (Quaas and Pollak, 1980) may improve genetic evaluations relative to NCE by accounting for atypical conditions peculiar to a given herd. Bias may be reduced with models specified to explain factors unique to a herd and by using fixed-effect corrections and variance components based on information from that herd. Evaluations restricted to a single herd, however, ignore performance of related animals in other herds and result in herd-specific definitions of the base. Thus, the value of within-herd predictions may be limited when selecting animals for use in other herds.

To provide insight on the relative merit of within-herd and across-herd evaluations of animals in a unique population, data from four herds based on Miles City Line 1 Hereford breeding were analyzed to 1) compare estimates of genetic and environmental variance and predictions of genetic merit from within-herd, across-herd and national cattle evaluations, and 2) assess the influence of different methods to account for effects of inbreeding, sex, and age of dam on predictions of genetic merit.

[1]This research was conducted under a cooperative agreement between USDA, ARS, and the Montana Agric. Exp. Sta. and is published as contribution no. J-4030 from the Montana Agric. Exp. Sta.

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Received August 21, 1995.
Accepted February 20, 1996.

Table 1. Description of performance records used in within- and across-herd analyses

Trait	Herd[a]	Mean	(SD)	n	Years
Birth weight, kg					
	FK	35.8	(4.9)	5,346	1935–1991
	HV	36.6	(4.9)	1,648	1964–1991
	CH	41.1	(4.2)	1,166	1978–1991
	HH	40.0	(4.0)	1,428	1979–1991
Weaning weight, kg					
	FK	183.9	(31.1)	4,998	1935–1991
	HV	205.2	(33.1)	1,494	1964–1991
	CH	272.2	(44.2)	2,208	1974–1991
	HH	264.6	(41.8)	2,655	1967–1991
Postweaning gain, kg					
	FK	114.4	(65.6)	4,025	1935–1990
	HV	128.3	(38.6)	990	1976–1990
	CH	163.4	(61.3)	1,811	1974–1990
	HH	138.7	(55.1)	1,642	1967–1990

[a]FK = Fort Keogh Livestock and Range Research Laboratory, Miles City, MT; HV = Montana Agricultural Experiment Station, Havre; CH = Cooper Hereford Ranch, Willow Creek, MT; HH = Holden Herefords, Valier, MT.

Materials and Methods

Data. The American Hereford Association (**AHA**) provided pedigree and performance records from four closely related herds. These herds were the original Miles City Line 1 herd at Fort Keogh (**FK**) Livestock and Range Research Laboratory, Miles City, MT, the Montana Agricultural Experiment Station herd at Havre (**HV**), and the seedstock herds of Cooper Hereford Ranch (**CH**) and Holden Herefords (**HH**). Records available from these herds are summarized in Table 1.

The FK herd was closed in 1934 and has been primarily selected for postweaning growth. History of the cattle, environment, management, and selection has been documented (Knapp et al., 1951; Brinks et al., 1965; Urick et al., 1966; MacNeil et al., 1992). The HV herd was established in 1962 by transfer of cattle from Miles City to Havre. Until 1975, selection was based on 365-d weight for HV males and 18-mo weight for HV females (Brinks and Knapp, 1975). Since 1975, HV based selection on the index of birth weight and yearling weight suggested by Dickerson et al. (1974). The HV herd was opened to outside Hereford sires in the 1988 through 1991 breeding seasons. Management and selection of the HV herd are described by Anderson et al. (1985, 1991).

Both CH and HH obtained breeding stock from the FK herd in the late 1940s and have periodically purchased FK bulls. Animals have also been exchanged between these two herds. Cooper Hereford Ranch, Willow Creek, MT, grazed irrigated and improved dryland pastures. Cows and heifers were wintered together and were provided hay before calving. At calving, from mid-January through February, first calf heifers were separated from the older cows and provided additional feed. Protein supplementation was provided before the April and May breeding season. The 60-d natural mating season occurred on dryland pastures. Single-sire pastures were used, with heifers separated from cows with calves. In July, bull calves and their dams were moved to irrigated pastures where they remained until weaning. Heifer calves and their dams were sometimes moved to irrigated pastures several weeks after the bulls. After weaning in October, bull calves were placed on a feedlot test with a grain and silage diet to allow approximately 1.3 kg/d gain. Heifer calves were placed on dryland pasture with supplemental feed to allow approximately .9 kg/d gain until the start of the breeding season.

Holden Herefords, Valier, MT, was dependent on irrigated and subirrigated pastures as sources of grazed forage. The HH calving, breeding, and weaning schedule was similar to that of CH. Other features of management were similar, although HH used subirrigated pastures rather than dryland. The move from subirrigated to more productive irrigated pastures occurred in August, with bulls and heifers moved at the same time. The bull test diet included concentrate and ad libitum access to hay.

Pedigrees of cattle with performance records were traced up to five generations before the 1934 establishment of Line 1 (MacNeil et al., 1992). The pedigrees used in analyses represented 14,336 animals, with 12,252 having performance records. All parents and all but three grandparents of animals with performance records were known. This pedigree information was used in all within- and across-herd analyses. Due to relationships and movements of animals among these herds, potentially important pedigree ties may have been eliminated by alteration of pedigree information specifically for within-herd analyses.

Performance records were edited to eliminate observations from all twin-born calves and observations with questionable weaning or yearling weigh dates and ages. Records on file were used to resolve irregularities in a small number of American Hereford Association pedigree and performance records. All acceptable performance records were used in across-herd analyses. Each within-herd analysis considered performance records only from that herd.

Analyses. To quantify the degree of relationship among the four herds, estimates of the genetic relationships among herds were derived by calculating what the average inbreeding coefficient would have been among hypothetical progeny resulting from drawing a random sample of 500 individuals from one herd randomly mated to a similarly drawn sample from another herd. This random sampling and mating process was repeated for each pair of herds.

Birth weight (**BWT**), weaning weight (**WWT**) and adjusted 160-d postweaning gain (**PWG**) were considered in separate within- and across-herd analyses to estimate genetic and environmental variances and predict individual breeding values. Variations of the following model were used:

$$y = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_d\mathbf{u}_d + \mathbf{Z}_m\mathbf{u}_m + \mathbf{Z}_{pe}\mathbf{u}_{pe} + \mathbf{e}$$

with an assumed (co)variance structure of:

$$\mathrm{Var}\begin{bmatrix}\mathbf{u}_d\\ \mathbf{u}_m\\ \mathbf{u}_{pe}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{A}\sigma^2_d & \mathbf{A}\sigma_{dm} & 0 & 0\\ \mathbf{A}\sigma_{dm} & \mathbf{A}\sigma^2_m & 0 & 0\\ 0 & 0 & \mathbf{I}_{pe}\sigma^2_{pe} & 0\\ 0 & 0 & 0 & \mathbf{I}_e\sigma^2_e\end{bmatrix},$$

where **y** is a vector of observations, **X** is a matrix relating a vector of fixed effects (β) to **y**, $\mathbf{Z}_d$ is an incidence matrix relating random direct additive genetic effects ($\mathbf{u}_d$) to **y**, $\mathbf{Z}_m$ relates random maternal additive genetic effects ($\mathbf{u}_m$) to **y**, $\mathbf{Z}_{pe}$ relates random maternal permanent environmental ($\mathbf{u}_{pe}$) effects to **y**, and **e** is a vector of random residual effects; **A** is the numerator relationship matrix among individuals, $\mathbf{I}_{pe}$ and $\mathbf{I}_e$ are identity matrices; σ^2_d, σ^2_m, σ^2_{pe}, and σ^2_e are direct additive genetic, maternal additive genetic, maternal permanent environmental, and residual variances, respectively; and σ_{dm} is the covariance between direct and maternal additive genetic effects. The model for PWG did not include terms for maternal additive or permanent environmental effects. Previous analysis of Line 1 data indicated that maternal additive and permanent environmental effects on PWG were not important (Tess and MacNeil, 1994).

The set of fixed effects considered in within-herd BWT analyses contained class effects of sex, age of dam, and contemporary group (**CG**) and linear effects of inbreeding of calf (F_c) and dam (F_d). Within-herd WWT analyses included these effects as well as the linear effect of age of calf. Fixed effects in within-herd PWG analyses were F_c and CG. Birth weight CG were defined by birth year, WWT CG by birth year and weaning weigh date, and PWG CG by sex, birth year, weaning weigh date, and yearling weigh date. Age of dam classes were 2, 3, 4, 5 to 9, and greater than 9 yr.

Variations of these sets of fixed effects were considered in across-herd BWT, WWT, and PWG analyses. Model 1 included within-herd effects of sex, age of dam, age of calf, F_c and F_d. Model 2 considered sex, age of dam, age of calf, and inbreeding effects pooled across herds. To determine the importance of accounting for effects of inbreeding in these genetic evaluations (Casanova et al., 1991), Model 3 also considered pooled sex, age of dam, and age of calf but ignored inbreeding. In these across-herd analyses, herd was included in definition of CG.

Two additional models were evaluated in across-herd analyses of adjusted weaning weight (**AWW**), with a priori adjustments for sex, age of calf, and age of dam (American Hereford Association, 1992) applied to weaning weight observations. Fixed effects for Model 4 AWW analysis were CG, F_c, and F_d. Model 5 AWW analysis included CG as the only fixed effect. Contemporary groups for AWW analyses were herd, birth year, weaning weigh date, and sex combinations. Effects considered by these models are listed in Table 2.

Estimates of genetic and environmental variance were computed using MTDFREML (Boldman et al., 1993). Variance components for BWT, WWT, and PWG were estimated in within-herd analyses of each herd. Across-herd variance component analyses of BWT, WWT, and PWG were conducted with Models 1, 2, and 3. Likelihood ratio tests (e.g., Visscher et al., 1991) were conducted to test for differences between each set of within-herd parameter estimates and the across-herd set of parameters estimated with Model 1. These tests compared log-likelihoods of within-herd analyses using within-herd parameter estimates with within-herd analyses using Model 1 parameter estimates. Variance components were not estimated with Models 4 or 5, used to analyze AWW.

Predictions of individual genetic merit were computed using the Animal Breeder's Toolkit (ABTK; Golden et al., 1992) to assemble and solve mixed model equations (Henderson, 1973). These within- and across-herd analyses used variance component estimates from the corresponding REML analyses. The Model 4 AWW analysis, with inbreeding regressions, used Model 2 WWT variance component estimates, and the Model 5 AWW analysis, without inbreeding, used the Model 3 WWT estimates. Expected progeny differences computed in these analyses were compared with EPD from the fall 1994 AHA NCE. Comparisons were based on product-moment correlations between sets of within-herd, across-herd, and NCE EPD and genetic trends predicted by these sets of EPD. The NCE used records of animals enrolled in the AHA Total Performance Records

Table 2. Effects[a] included in models used for within- and across-herd analyses

Model	Linear effects	Class effects	Random effects
Within-herd			
Birth weight	F_c, F_d	Sex, AOD, CG	u_d, u_m, u_{pe}
Weaning weight	F_c, F_d, AOC	Sex, AOD, CG	u_d, u_m, u_{pe}
Postweaning gain	F_c	CG	u_d
Across-herd			
Model 1			
Birth weight	Herd × (F_c, F_d)	Herd × (sex, AOD), CG	u_d, u_m, u_{pe}
Weaning weight	Herd × (F_c, F_d, AOC)	Herd × (sex, AOD), CG	u_d, u_m, u_{pe}
Postweaning gain	Herd × F_c	CG	u_d
Model 2			
Birth weight	F_c, F_d	Sex, AOD, CG	u_d, u_m, u_{pe}
Weaning weight	F_c, F_d, AOC	Sex, AOD, CG	u_d, u_m, u_{pe}
Postweaning gain	F_c	CG	u_d
Model 3			
Birth weight		Sex, AOD, CG	u_d, u_m, u_{pe}
Weaning weight	AOC	Sex, AOD, CG	u_d, u_m, u_{pe}
Postweaning gain		CG	u_d
Model 4			
Adjusted weaning weight[b]	F_c, F_d	CG	u_d, u_m, u_{pe}
Model 5			
Adjusted weaning weight[b]		CG	u_d, u_m, u_{pe}

[a]F_c = inbreeding of calf; F_d = inbreeding of dam; AOD = age of dam (yr classes); CG = contemporary group (defined in text); u_d = additive direct effect; u_m = additive maternal effect; u_{pe} = permanent environmental effect; AOC = age of calf (d).
[b]Weaning weight adjusted for AOC and sex × AOD according to American Hereford Association (1992) procedures.

program since 1973 with EPD calculated using a reduced animal model (Quaas and Pollak, 1980).

Comparisons of EPD were made with animals jointly represented in national, within-herd, and across-herd evaluations. This excluded animals born before 1973 not represented in the NCE and those born since 1991 not included in within- and across-herd evaluations. For a specific herd, comparisons of within-herd, across-herd, and NCE EPD included only animals registered to that herd. The EPD comparisons included direct BWT, direct and maternal WWT, and PWG.

Results and Discussion

The four herds considered in this study differed in raw means for BWT, WWT, and PWG (Figure 1) and level of inbreeding (Figure 2). Birth weights in FK and HV were similar until the late 1980s and were less than in HH and CH. In the last years of data the four herds became more distinct, with FK having the lightest BWT, followed by HV, HH, and CH. A similar pattern was observed with WWT, although ranks of CH and HH were reversed. Phenotypic PWG trends showed less distinction among the herds, although HV consistently had the lowest mean PWG.

After formation of Line 1, inbreeding in FK accumulated rapidly due to mating close relatives (MacNeil et al., 1992). Since 1945, inbreeding in FK increased at a rate of .21%/yr. Inbreeding in the FK and HV herds was similar until the start of an outcrossing experiment at HV. The average inbreeding coefficient of HV calves was reduced to a level similar to that of HH and CH by the introduction of outside sires. Inbreeding levels in HH and CH remained about 15% less than in FK.

Estimates of the mean genetic relationship between herds (Table 3) ranged from .24 (CH and HH) to .44 (FK and HV). These between-herd relationships imply inbreeding levels of 12 to 22% would result from random mating of animals from the separate herds. Considering that these herds originated from essentially the same genetic stock and that pseudo-cross-herd matings indicate a relatively high degree of relationship among these herds, the herds might be considered four environmentally distinct instances of the same genetic population. As such, homogeneity of genetic (co)variances might be anticipated with any potential heterogeneity of variance arising due to environmental differences.

Variance Components. Within-herd variance component and parameter estimates were not the same across herds and did not seem related to level of phenotypic performance (Table 4). Likelihood ratio tests comparing each set of within-herd parameter estimates with Model 1 parameter estimates indicated differences in sets of parameters. Except for BWT in HV and PWG in FK, all sets of within-herd parameter estimates were different from across-herd Model 1 parameter estimates ($P < .05$). Given the apparent lack of relationship between phenotypic performance and variance component estimates, procedures to account for heterogenous phenotypic variances

Table 3. Estimates of mean genetic relationships among randomly selected individuals from different herds

Herd[a]	n	Herd HV	CH	HH
FK	5,391	.438 ± .082	.313 ± .073	.265 ± .092
HV	1,660		.321 ± .070	.278 ± .102
CH	2,416			.236 ± .076
HH	2,785			

[a]FK = Fort Keogh Livestock and Range Research Laboratory, Miles City, MT; HV = Montana Agricultural Experiment Station, Havre; CH = Cooper Hereford Ranch, Willow Creek, MT; HH = Holden Herefords, Valier, MT.

(Brotherstone and Hill, 1986; Visscher et al., 1991; Weigel and Gianola, 1993) or heterogenous genetic and environmental variances due to scaling (Quaas et al., 1989) may not be adequate. Application of more computationally intense methods to allow heterogenous variances (Gianola et al., 1992; Weigel and Gianola, 1992; San Cristobal et al., 1993) may be warranted, but feasibility of these methods with large data sets and multi-component models is limited. Also, reliability of simultaneously estimated within-herd variance components is restricted by limited data (Winkelman and Schaeffer, 1988).

Table 4. Variance component and parameter estimates from within-herd, across-herd and American Hereford Association national cattle evaluations (NCE)

		(Co)variance components[a]					Parameter estimates[b]			
Trait	Herd	σ^2_d	σ^2_m	σ_{dm}	σ^2_{pe}	σ^2_e	h^2	m^2	r_{dm}	c^2
Birth weight										
	FK*	6.3	2.9	.6	.2	11.1	.30	.14	.13	.01
	HV	11.6	2.8	.2	.7	7.4	.51	.12	.04	.03
	CH*	8.9	.4	−.3	1.5	5.6	.55	.03	−.14	.09
	HH*	8.1	2.2	.1	.3	5.3	.50	.14	.03	.02
	M1[c]	7.0	2.4	.4	.5	9.4	.36	.12	.09	.03
	M2[d]	6.7	2.5	.5	.5	9.5	.34	.13	.12	.02
	M3[e]	7.0	2.5	.4	.5	9.5	.35	.12	.10	.03
	NCE	6.3	2.3	−1.1	.5	5.2	.49	.18	−.27	.04
Weaning weight										
	FK*	85.5	113.3	−7.8	68.5	231.3	.17	.23	−.08	.14
	HV*	103.7	56.7	10.1	137.7	216.9	.20	.11	.13	.26
	CH*	124.2	110.8	−26.3	64.8	395.2	.19	.17	−.22	.10
	HH*	160.3	111.5	−25.2	113.2	174.1	.30	.21	−.19	.21
	M1	133.6	103.6	−16.5	89.7	238.5	.24	.19	−.14	.16
	M2	136.5	115.2	−19.4	83.8	294.9	.22	.19	−.15	.14
	M3	113.0	118.7	−20.7	85.6	297.7	.22	.19	−.16	.14
	NCE	123.5	119.8	−34.1	11.8	288.3	.24	.23	−.28	.02
Postweaning gain										
	FK	77.7	—	—	—	241.4	.24	—	—	—
	HV*	176.2	—	—	—	190.1	.48	—	—	—
	CH*	125.5	—	—	—	257.0	.33	—	—	—
	HH*	94.8	—	—	—	196.6	.33	—	—	—
	M1	99.1	—	—	—	232.8	.30	—	—	—
	M2	98.1	—	—	—	233.5	.30	—	—	—
	M3	97.0	—	—	—	235.6	.29	—	—	—
	NCE	85.6	—	—	—	276.6	.24	—	—	—

[a]kg^2, σ^2_d = direct additive genetic variance; σ^2_m = maternal additive genetic variance; σ_{dm} = covariance of direct and maternal additive genetic effects; σ^2_{pe} = permanent environmental variance due to dams; and σ^2_e = residual variance.

[b]$\sigma^2_p = \sigma^2_d + \sigma^2_m + \sigma_{dm} + \sigma^2_{pe} + \sigma^2_e$; $h^2 = \sigma^2_d/\sigma^2_p$; $m^2 = \sigma^2_m/\sigma^2_p$; $r_{dm} = \sigma_{dm}/\sqrt{\sigma^2_d\sigma^2_m}$; and $c^2 = \sigma^2_{pe}/\sigma^2_p$.

[c]Across-herd analysis with herd-specific sex, age of dam and inbreeding effects.

[d]Across-herd analysis with sex, age of dam and inbreeding effects pooled across herds.

[e]Across-herd analysis with sex and age of dam effects pooled across herds and inbreeding ignored by model.

*−2 (difference in log-likelihood) of within-herd analysis using within-herd parameter estimates and within-herd analysis using across-herd (Model 1) parameter estimates significant at $P < .05$.

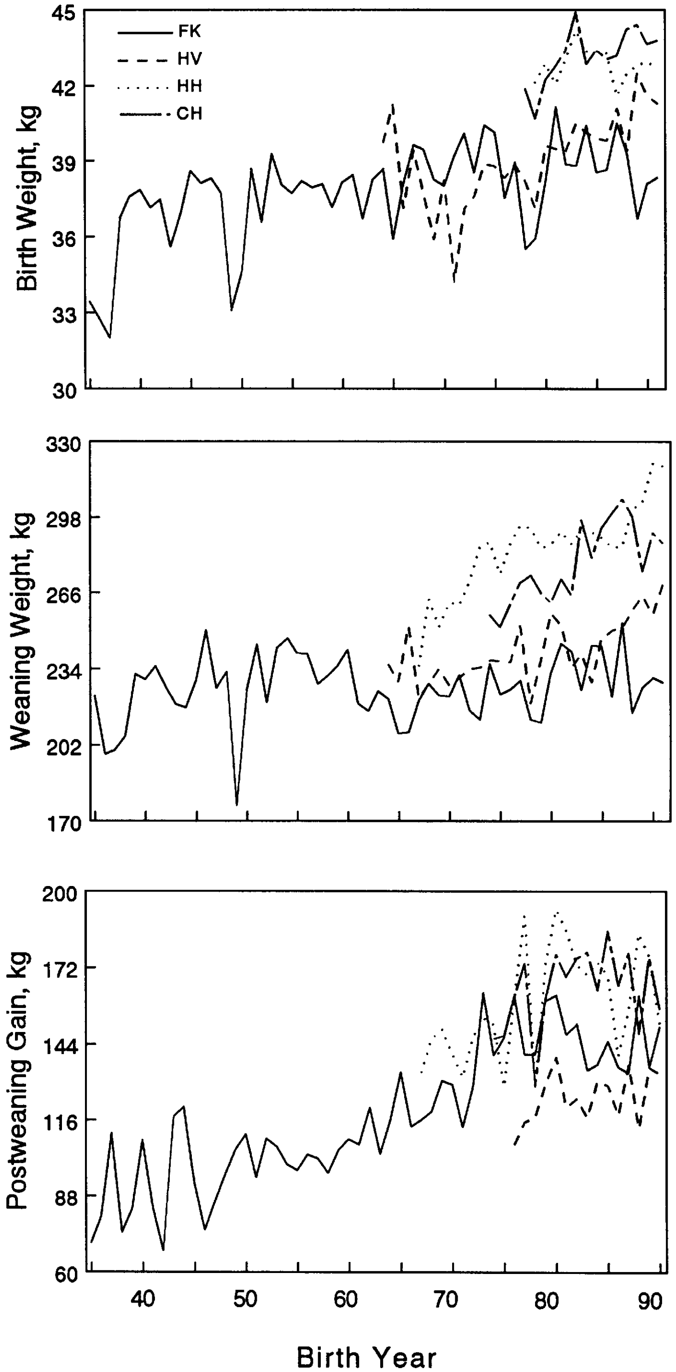

Figure 1. Means by birth year for birth weight, weaning weight, and postweaning gain for four Miles City Line 1 Hereford herds.

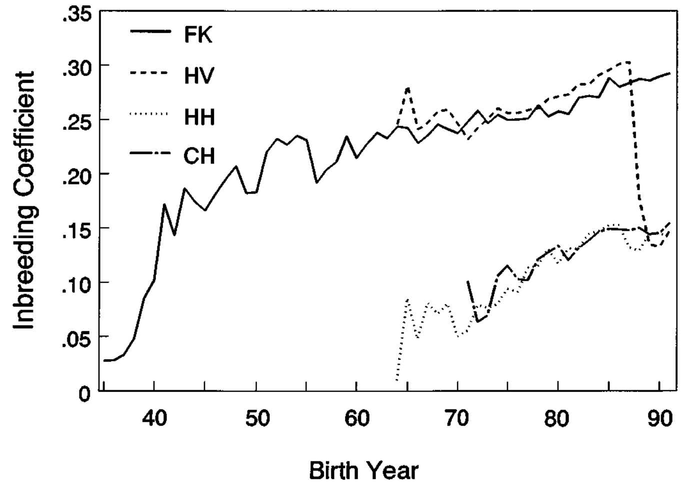

Figure 2. Mean inbreeding coefficients by birth year of four Miles City Line 1 Hereford herds.

Variance components estimated from the across-herd analyses with Models 1, 2, and 3 were similar. Model 1, with herd-specific class effects and linear regressions, resulted in the numerically smallest estimates of σ_e^2, and r_{dm} estimates closest to zero. The slight differences among estimates obtained with the different models are not likely to be important.

There was general agreement between across-herd and NCE estimates of direct and maternal additive genetic variances, although some discrepancy in estimates of direct-maternal covariances, maternal permanent environmental variances, and environmental variance were found (Table 4). The most notable differences between across-herd Model 3 estimates and NCE estimates were for BWT σ_{dm} (.4 vs −1.1 kg^2), BWT σ_e^2 (9.5 vs 5.2 kg^2), and WWT σ_{pe}^2 (85.6 vs 11.8 kg^2).

Fixed effects. Best linear unbiased estimates (**BLUE**) of inbreeding, sex, and age of dam effects obtained with Model 2 for within-herd and across-herd analyses are presented in Table 5. Adjustment factors calculated from AHA (1992) regression equations are also presented for comparison. Herd-specific effects estimated with Model 1 for across-herd analyses were essentially the same as from within-herd analyses. Pooled estimates of sex, age of dam, and age of calf effects were not influenced by ignoring inbreeding in Model 3. For all herds but CH, BWT analyses indicate inbreeding depression due to F_c ($P < .05$) but not F_d. This is consistent with results of MacNeil et al. (1992), who used a subset of the FK data included in this study. In contrast to MacNeil et al. (1992), who found an insignificant regression for F_c on preweaning daily gain, both F_c and F_d regressions for WWT were significant in FK ($P < .01$). This study included 571 WWT records of calves in a subline selected for increased YWT with below-average BWT that were not used by MacNeil et al. (1992). Also, MacNeil et al. (1992) reported results for preweaning daily gain, which did not include BWT, whereas WWT includes BWT and preweaning gain. Brinks and Knapp (1975) also reported significant F_c and F_d effects on WWT of FK male calves, with the magnitude of the F_d regression greater than that for F_c. Regressions of F_c on WWT were important in all herds and in the combined analysis, but F_d regressions were important

Table 5. Estimates of effects of inbreeding of calf, inbreeding of dam, sex, age of calf, and age of dam from within-herd and across-herd pooled analyses and American Hereford Association (AHA) adjustment factors

	Herd[a]					
	FK	HV	CH	HH	Pooled[b]	AHA[c]
Birth weight						
Inbreeding, kg/1% inbreeding						
Calf	−.084 ± .018	−.069 ± .032	.010 ± .046	−.114 ± .042	−.085 ± .014	—
Dam	−.018 ± .018	−.025 ± .034	−.012 ± .038	−.09 ± .036	−.025 ± .014	—
Sex (difference from heifer, kg)						
Bull	−2.6 ± .11	−2.2 ± .19	−3.0 ± .32	−2.5 ± .17	−2.5 ± .08	—
Age of dam (difference from AOD 5, kg)						
2	−4.7 ± .22	−4.7 ± .27	−2.9 ± .34	−2.7 ± .30	−4.1 ± .14	2.3
3	−1.9 ± .15	−2.2 ± .27	−1.6 ± .30	−.5 ± .32	−1.8 ± .11	.9
4	−.7 ± .15	−.3 ± .28	−.8 ± .30	.3 ± .27	−.5 ± .11	0
>9	−2.0 ± .54	−2.0 ± .50	−2.6 ± 2.0	.6 ± 1.5	−1.9 ± .34	.9
Weaning weight						
Calf age, kg/d	.95 ± .02	.91 ± .04	.91 ± .03	.95 ± .02	.95 ± .01	*[c]
Inbreeding, kg/1% inbreeding						
Calf	−.429 ± .086	−.551 ± .144	−.689 ± .215	−.391 ± .140	−.490 ± .070	—
Dam	−.482 ± .103	−.445 ± .193	−.035 ± .230	−.151 ± .181	−.380 ± .084	—
Sex (difference from heifer, kg)						
Bull	13.2 ± .5	14.1 ± 1.0	54.1 ± 1.1	23.5 ± 1.6	23.3 ± .5	—
Steer	2.4 ± 1.0	—	7.0 ± 5.5	−9.1 ± 4.2	4.1 ± 1.0	—
Age of dam (difference from AOD 5, kg)						
2	−40.5 ± 1.1	−37.2 ± 1.5	−18.5 ± 1.7	−21.4 ± 1.3	−30.6 ± .7	27.7
3	−17.8 ± .8	−17.4 ± 1.4	−11.3 ± 1.5	−9.3 ± 1.2	−15.1 ± .6	15.4
4	−6.0 ± .7	−6.3 ± 1.4	−3.6 ± 1.5	−1.3 ± 1.1	−4.6 ± .6	6.8
>9	−16.1 ± 2.6	−21.8 ± 2.5	−12.2 ± 11.6	−8.7 ± 4.1	−16.4 ± 1.8	3.6
Postweaning gain						
Inbreeding, kg[b]/1% inbreeding						
Calf	−.341 ± .080	−.866 ± .181	−.376 ± .181	−.158 ± .149	−.405 ± .063	—

[a]FK = Fort Keogh Livestock and Range Research Laboratory, Miles City; HV = Montana Agricultural Experiment Station, Havre; CH = Cooper Hereford Ranch, Willow Creek; HH = Holden Hereford, Valier.

[b]Across-herd analysis with sex, age of dam, and inbreeding effects pooled across herds (Model 2).

[c]American Hereford Association (1992) weaning weight adjustment factors are calculated from quadratic regressions on age of dam (d) and cubic regressions on age of calf (d). The values shown are appropriate for 205-d-old non-creep-fed bull calves with dams that are 730 d (2-yr-old), 1095 d (3-yr-old), 1460 d (4-yr-old), and 3650 d (10-yr-old).

only for FK, HV, and the combined analysis. Inbreeding of calf influenced PWG in all analyses except HH.

Differences in BWT of bull and heifer calves ranged from 2.2 kg in HV to 3.0 kg in CH, with bulls 2.5 kg heavier than heifers in the combined analysis. The difference of 2.6 kg in FK is similar to the 2.5-kg difference in FK calves found by Koch and Clark (1955) and MacNeil et al. (1992). Sex differences were less consistent for WWT, with bulls ranging from 13.21 kg (FK) to 54.05 kg (CH) heavier than heifers. The relatively large difference in CH may be attributed to bull calves being moved to irrigated pastures earlier than heifers, and points out the necessity of accounting for differential management by sex.

In all BWT analyses, differences between 2-yr-old and 5- to 10-yr-old dams are somewhat greater than those used by the American Hereford Association (1992). Estimates of pooled age of dam effects on WWT are in agreement with American Hereford Association. Differences in age of dam effects for BWT and WWT are greatest in FK and HV. Because these two herds have the highest levels of inbreeding, the magnitude of age of dam effects may be a manifestation of delayed maturity due to inbreeding (Nelson and Lush, 1950; Dinkel et al., 1972). Differences in management may also affect estimates of age of dam effects. In FK and HV, 2-yr-old dams were managed with older cows, whereas 2-yr-olds were separated from the rest of the cow herd and received different treatment at CH and HH.

Genetic predictions. Genetic trends for each herd for BWT direct (Figure 3), WWT direct (Figure 4), WWT maternal (Figure 5), and PWG (Figure 6) are depicted. For each herd and trait the trends obtained with different data and models show general agreement in year-to-year fluctuations. Differences among within-herd, across-herd, and NCE trends may partially be attributed to differences in data available for each analysis. Because the same pedigree and performance information was used by the three across-herd models, differences in across-herd trends are attributable to differences in biology described by each model.

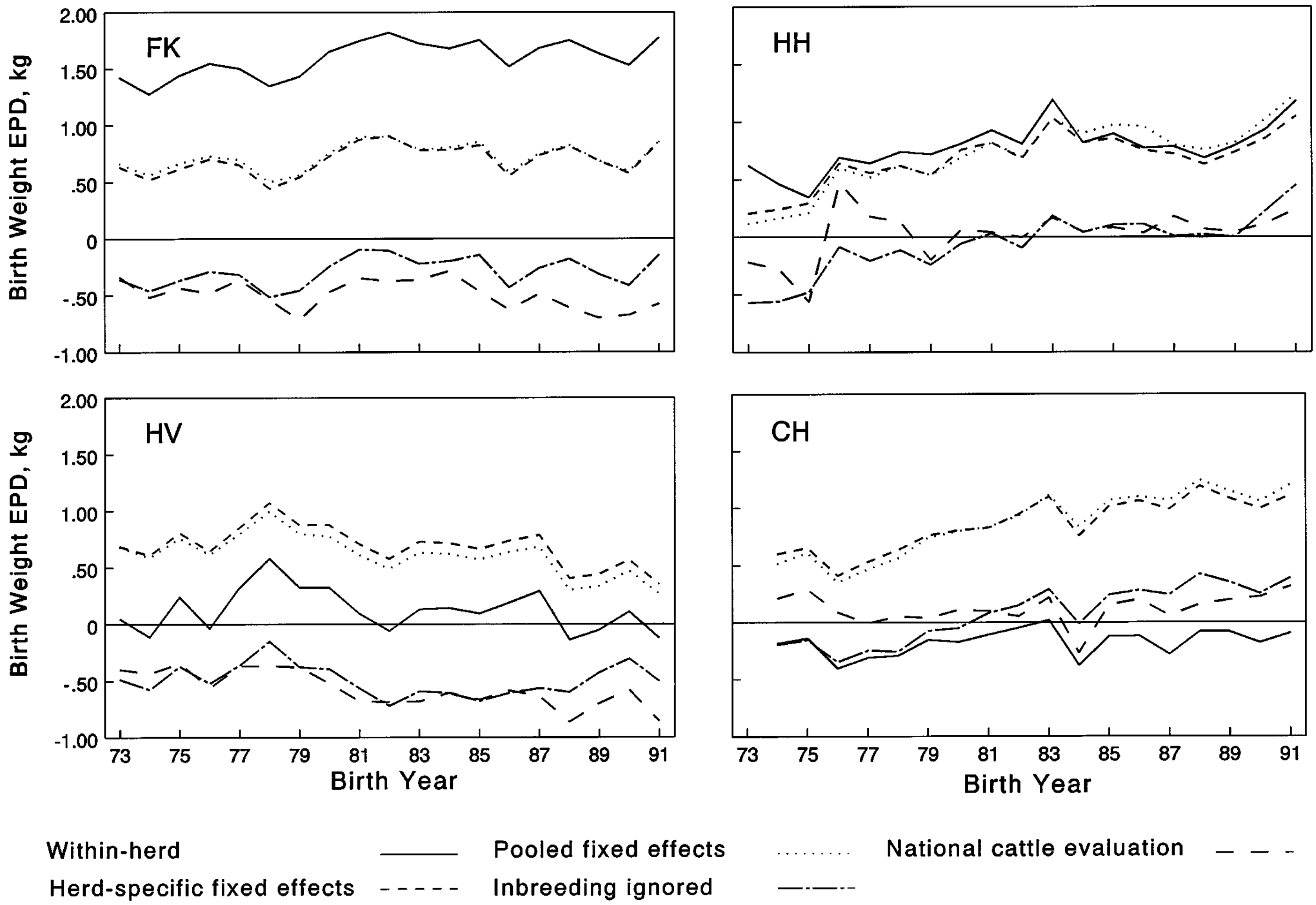

Figure 3. Genetic trends for birth weight for four Miles City Line 1 Hereford herds estimated from within-herd, across-herd, and national cattle evaluations.

Table 6. Correlations among across-herd and national cattle evaluation direct and maternal weaning weight expected progeny difference

		Analysis				
Effect	Analysis[a]	M2	M3	M4	M5	NCE
Weaning weight direct effect						
	M1	.936	.864	.963	.859	.671
	M2		.958	.945	.872	.660
	M3			.894	.932	.682
	M4				.924	.700
	M5					.725
Weaning weight maternal effect						
	M1	.952	.915	.923	.870	.684
	M2		.967	.946	.899	.690
	M3			.892	.953	.743
	M4				.915	.692
	M5					.781

[a]M1 = across-herd analysis with herd-specific sex, age of dam and inbreeding effects; M2 = across-herd analysis with sex, age of dam and inbreeding effects pooled across herds; M3 = across-herd analysis with sex and age of dam effects pooled across herds and inbreeding ignored; M4 = across-herd analysis with AHA-recommended a priori adjustments to weaning weight and inbreeding included in model; M5 = across-herd analysis with AHA-recommended a priori adjustments to weaning weight and inbreeding ignored.

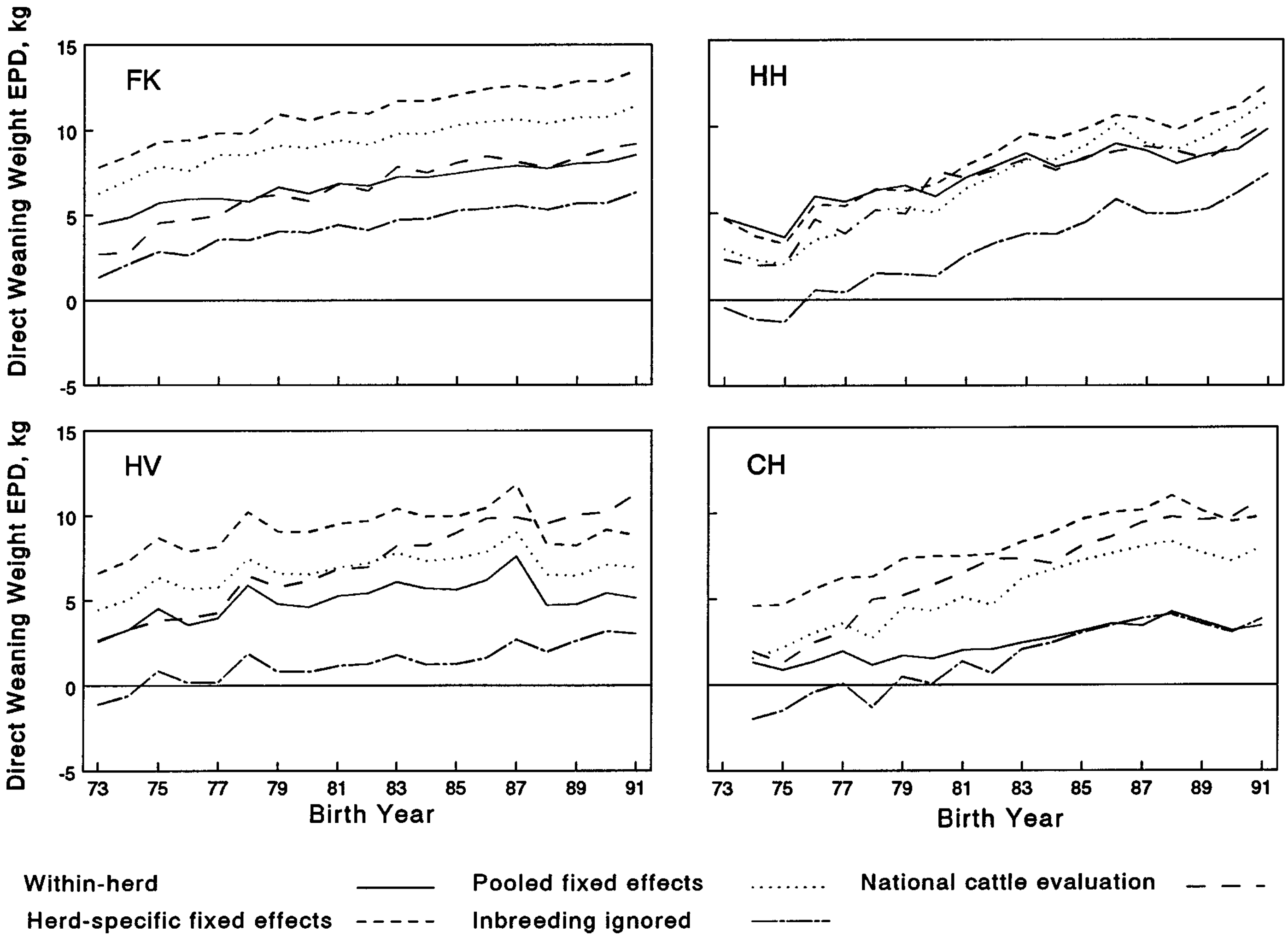

Figure 4. Direct genetic trends for weaning weight for four Miles City Line 1 Hereford herds estimated from within-herd, across-herd, and national cattle evaluations.

Comparison of across-herd trends suggests adjustment for inbreeding affects genetic evaluations. For direct and maternal WWT and PWG, rates of increase in genetic trends estimated from evaluations that disregarded inbreeding (Model 3) were less than increases estimated from Model 2, which included inbreeding. Consideration of pooled or herd-specific fixed effects had no influence on PWG trends but did affect estimated gains in direct BWT and direct and maternal WWT trends. Analysis with fixed effects pooled across herds resulted in faster estimated rates of increase in direct and maternal WWT for FK and HV, but slower estimated change in direct and maternal WWT for CH and HH.

Product-moment correlations between Model 1 and within-herd EPD ranged from .89 for maternal WWT at HH to .99 for direct BWT at FK. In contrast, correlations between Model 1 and NCE EPD ranged from .67 for direct WWT to .79 for direct BWT. Model 3 EPD, with pooled fixed effects and inbreeding ignored, were more highly correlated with NCE EPD than across-herd EPD obtained with inbreeding accounted for by direct and maternal regressions.

For weaning weight, correspondence of within-herd to across-herd evaluations was consistently greatest with Model 1, which included herd-specific fixed effects. As indicated by Table 6, EPD from models that included inbreeding (Models 2 and 4) showed greater agreement with the herd-specific model (Model 1) than corresponding models that ignored inbreeding (Models 3 and 5). Correlations between NCE EPD and across-herd direct and maternal EPD for WWT (Models 1, 2, and 3) or AWW (Models 4 and 5) increased with resemblance of analytical procedures to NCE procedures. Predictions from models that ignored inbreeding (Models 3 and 5) agreed most with NCE EPD, with the most pronounced differences observed in maternal EPD. The highest correlations with NCE EPD were obtained with Model 5, which was most similar to NCE procedures due to omission of inbreeding effects and use of a priori AHA adjustments to weaning weight. These correlations suggest that if

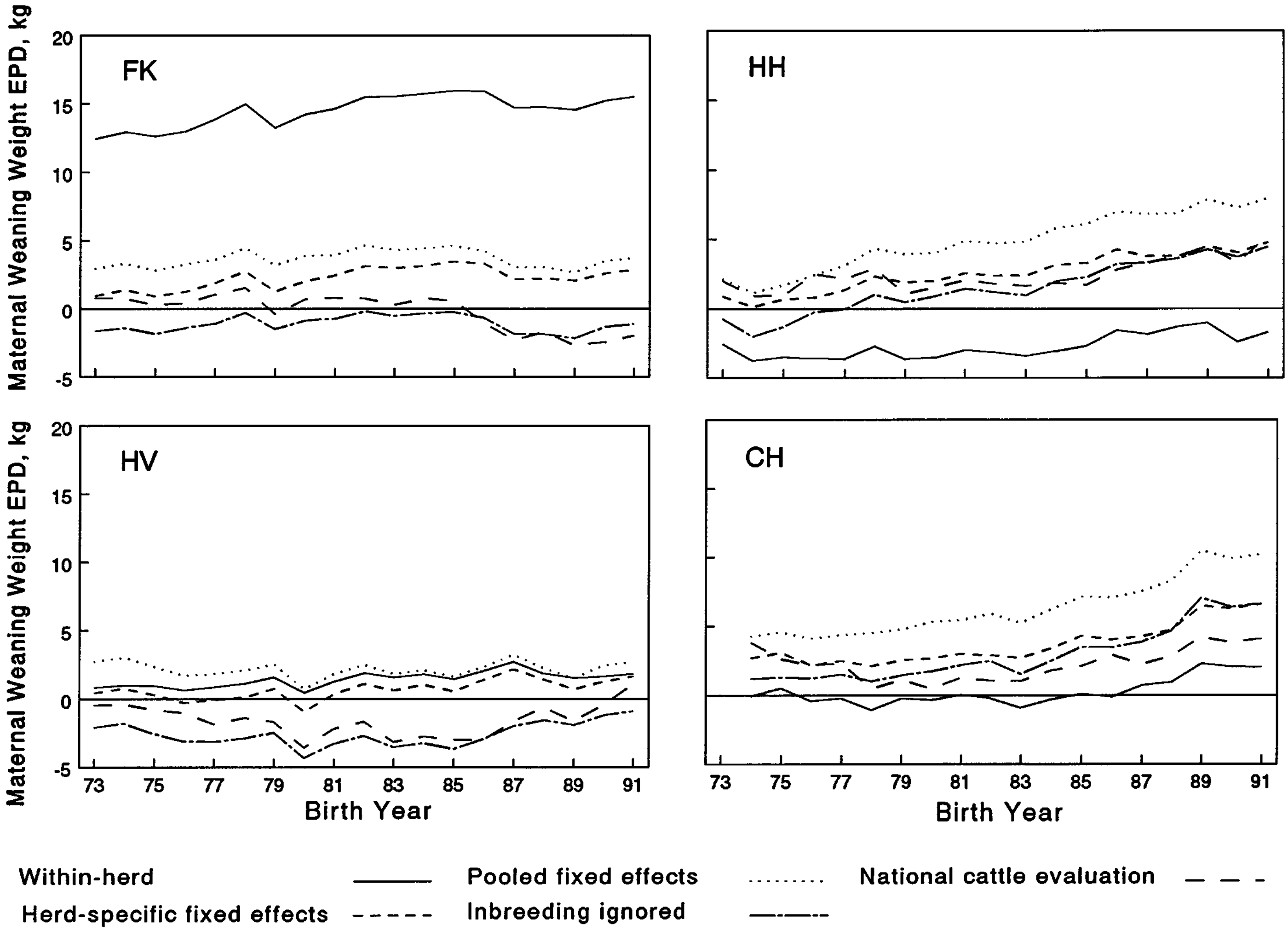

Figure 5. Maternal genetic trends for weaning weight for four Miles City Line 1 Hereford herds estimated from within-herd, across-herd, and national cattle evaluations.

predictions from the herd-specific model (Model 1) most accurately represent true breeding values, predictions from less highly specified models will be less accurate. Genetic progress with selection based on the less accurate predictions, including NCE EPD, may be slower than that possible using more accurate predictions from models with more highly specified fixed effects.

General discussion. Results of this study suggest important herd differences in effects of common fixed factors and the possibility of heterogenous genetic and environmental variances, even with high genetic relationships between herds. Methods used to deal with these differences have a substantial impact on predictions of genetic merit. Within-herd evaluation is feasible to allow a high degree of detail in specification of fixed effects and variance components, but utility may be limited to selection of replacement animals from within that herd. Without information from other sources, within-herd evaluations have little value to compare and select animals from different herds.

Across-herd evaluations, particularly NCE, provide basis for selection among different herds. Methods currently used by NCE may not adequately address adjustments for management and environmental factors unique to an individual herd. This may result in unfair evaluations of animals in some herds, relative to other herds. A priori adjustments do not consider interactions with environment, and procedures used to obtain data from breeders may limit the ability of NCE to address some management factors. Management codes on reporting forms may not be sufficiently flexible to allow formation of appropriate contemporary groups. Even when designation of calves managed alike is possible, breeders may overlook or be unaware of the need to specify appropriate management groups. The effects of inbreeding on animal performance should also be considered in genetic evaluation, especially in NCE of breeds with levels of inbreeding that might result from extensive use of linebreeding by some breeders.

Because fully addressing differences in individual herds with NCE is not likely to become feasible,

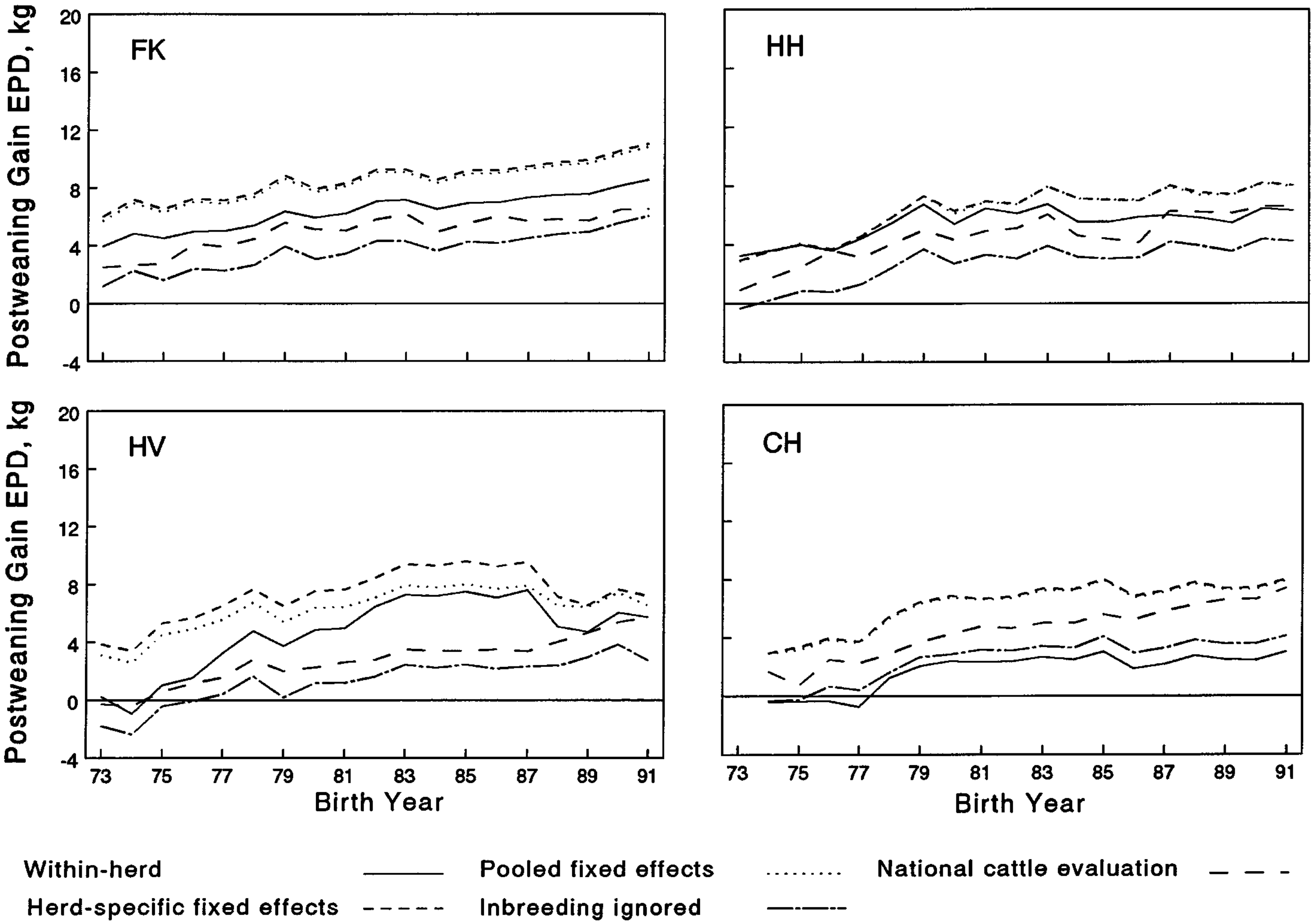

Figure 6. Genetic trends for postweaning gain for four Miles City Line 1 Hereford herds estimated from within-herd, across-herd, and national cattle evaluations.

exploration of within-herd analysis methods that incorporate information from outside sources is suggested. Henderson (1975) and Slanger et al. (1976) described an approach to incorporate AI sire evaluations into intraherd genetic predictions for dairy cows. Analagous methodology may be useful with beef cattle to incorporate NCE results into within-herd analyses to more reliably predict progeny performance subject to the unique management and environment of individual herds.

Implications

Even with the inability of current national cattle evaluation to address uniqueness of individual herds, those expected progeny differences are the most reliable tool available to compare and select animals from different herds. National cattle evaluations may be improved by allowing for within-herd differences in effects of factors such as sex, age of dam, and inbreeding. Within-herd genetic evaluations do not include enough information to be reliable for selection outside that herd. Further research to develop methods that incorporate results of national cattle evaluation into within-herd analyses to obtain expected progeny differences that are more applicable to that herd is suggested.

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